Computer Methods and Programs in Biomedicine 212 (2021) 106457

Contents lists available at ScienceDirect

Computer Methods and Programs in Biomedicine

journal homepage: www.elsevier.com/locate/cmpb

Profeel—An open source dosimetry data visualization and analysis software

Tomppa Pakarinen[a,b,*], Jarkko Ojala[a]

[a] Department of Medical Physics and Department of Oncology, Tampere University Hospital, Tampere, Finland
[b] Faculty of Medicine and Health Technology, Tampere University, Tampere, Finland

ARTICLE INFO

Article history:
Received 30 April 2021
Accepted 11 September 2021

Keywords:
Dosimetry
Matlab
Radiotherapy
Quality assurance

ABSTRACT

Background and objectives: This article presents Profeel, a Matlab (MathWorks Inc., MA) based open source dosimetry data visualization and analysis software. Profeel aims to support quality assurance, dosimetry and research in the field of radiotherapy by providing an environment to visualize, process and analyse measured and simulated dosimetry data from several data sources used in radiotherapy practice and research.

Methods: The processing and analysis tools are based on routinely used dosimetry analysis methods, such as gamma analysis, different data normalizations and data filtering. Additionally the Profeel performs an automatic 1 dimensional profile and percentage depth dose analysis in accordance with International Electrotechnical Commission definitions. All data can be operated by user created custom functions and lower dimensionality data can be extracted from volume doses and dose planes.

Results: Profeel supports data import in all 3 dimensions and offers an intuitive user interface to perform data visualization, processing and analysis between simulated and measured data. Profeel and its source code are distributed free of charge under the General Public Licence (GPL).

Conclusions: Profeel has shown to be an agile tool for fulfilling various needs of several researchers and since Profeel is under constant development and is an open source project, community needs, issues and bug reports are taken into account in the development.

1. Introduction

In radiotherapy (RT), the radiation dose determination is essential in assuring an accurate treatment delivery, maximizing the potential health benefit and minimizing the possibility for a potential adverse health effect to the patient. Dose determination can be done through dosimetric measurements (dosimetry) and dose calculations. In modern RT, three dimensional (3D) dose distributions are to be determined by default, from which two dimensional (2D) and one dimensional (1D) data sets are extracted for further analysis and use. Also, in measurements, often 1D and/or 2D data can be directly acquired.

No matter which method is utilized in dose determination, there are always various sources of uncertainty involved. In dosimetry, the equipment, especially the detector, introduces intrinsic and extrinsic factors that add to the combined uncertainty, if left uncorrected. These include volume averaging due to finite size of the active volume, energy and directional dependence etc. Also, the measured results always represent a single sample of the output of the device producing the radiation beam to be measured. In dose calculation the challenges are usually related to the approximations in the underlying dose calculation algorithm simulating the radiation transport in matter.

Thus, to achieve high quality data and high level of confidence in dose determination, it is essential to combine data from various sources, taking into account their related uncertainties. This requires the comparison of data, but often the software for data visualization and analysis support only the data format from the measurement device manufacturer itself and even if general purpose data formats are supported, lots of pre-processing is required prior to successful import. Therefore, in this work, we have developed a software, that supports measurement data formats from several dosimetry device manufacturers, general dose distribution data format used in clinical RT treatment planning systems (TPS) (DICOM-RT) and Monte Carlo dose calculation data format (EGSnrc/3ddose), which are often used for independent validation of dose distributions.

* Corresponding author at: Postal: Tampereen yliopistollinen sairaala Sädehoitoyksikkö PL 2000 33521 Tampere, Finland.
E-mail address: Tomppa.pakarinen@tuni.fi (T. Pakarinen).

https://doi.org/10.1016/j.cmpb.2021.106457

There are few published works considering open source programs and tools for radiotherapeutic dosimetry data analysis. Programs, such as Computational Environment for Radiological research (CERR) [1] SlicerRT radiation therapy toolkit for 3D slicer [2] and XSTING [3] are developed tools for radiotherapeutic research purposes, but do not support measured data import and thus, computed and measured data comparison. Other published dosimetry and dose calculation software often require custom measurement setups [4], are intended on fields outside of radiotherapy [5] or focus on radiotherapy treatment planning and optimization [6,7], and rarely supply the source code. Unpublished work such as 3ddose-tools (.3ddose) [8] and web-based VICTORIA (.3ddose, .dcm, .egsphant) [9] allow the user to import, visualize and plot computed data but unfortunately do not support measured data formats. At the time and until today, to the best of our knowledge, there are no existing open-source programs to visualize, process and analyze the required source data (see section 3.1) from a dosimetric standpoint.

2. Methods

Profeel v. 1.17 is programmed completely with Matlab (R2020a v. 9.8), utilising graphical user interface development environment GUIDE creation library, Image Processing™, Signal Processing™ and Parallel Computing™ Toolboxes. Matlab is used extensively in radiotherapy research, with a variety of build-in Toolboxes and functions for DICOM and other technical extensions. Profeel combines dosimetry data visualization with processing and analytics tools in an intuitive and easy to use user interface (UI). Profeel has a number of data processing and analytic UI tools, and the details of the computationally most relevant methods are described in detail below.

2.1. Processing during import and data extraction

First, all imported data is combined into a structure set with predefined fields. The main data structure consists of sub structures containing the raw data, interpolated data, data normalizations as matrices with corresponding position vectors. Additionally, result fields, reference to parent structure and metadata, are included in the structure. Visualization of the imported data, especially for large 3D datasets, requires processing time. To reduce the wait time during visualization, a lower resolution dataset is automatically computed and added to the structure, if the original resolution exceeds a predefined hard-coded value of 120 data points per axis, which was considered as a good compromise between visual details and computing performance. The low resolution dataset is used only to speed up visualization, and as the default option for gamma index, distance to agreement (DTA) and dose difference (DD) computation, when the low resolution option is activated.

2.2. Interpolation methods

Imported 1D and 2D data are automatically interpolated with linear interpolation to 10 times the original resolution, i.e. values are added linearly between successive data points, preserving the original points. Interpolated data is then added to the data structure. 3D data is not interpolated during import, apart from lower resolution interpolation. The interpolated data is used as the default data source for profile and PDD parameters, and for 'brute force' method computations. Additionally, interpolated data is used as the source data in 'analytical method' computation for gamma parameters and lower dimension data extraction. Here the 'brute force' method refers to additional interpolation, finding the closest values in a numeric manner through linear interpolation, and 'analytical' refers to solving the line or plane cross sections analytically in cases where the initial linear interpolation sampling is not adequate, e.g. when lower dimension extraction is requested from a point that does not exist in the data structure. The user is prompted to wait during data import, since large dataset import times may be long (minutes). For .3ddose data type, the measurement uncertainty ('error' in Profeel) dataset can optionally be neglected, thus halving the import time. Otherwise the uncertainty data will be imported as default.

Data- and metadata structures are added to the main structure during lower dimension extraction, similar to the structure transformations during the data import. If the user-requested plane does not exist in 3D stack, Profeel interpolates the plane from the requested position. For analogous cases in 1D, Profeel finds the nearest existing points from the linearly interpolated data substructure.

2.3. Interactive profile

Quick profile is an interactive tool in Profeel, which allows the user to display and adjust 1D profiles from 2D data. In Profeel, 2D data structure is saved as $m\,x\,n$ matrix $\boldsymbol{M}$, where m and n correspond to the visualized 2D data dimensions, i.e. either the original or lower resolution data. A line $\boldsymbol{L}$, drawn within $\boldsymbol{M}$ consist of a starting point p_1 and and an endpoint p_2, which confine a submatrix $\boldsymbol{m}$, where $\boldsymbol{m}\subseteq\boldsymbol{M}$, and where the diagonal $diag(\boldsymbol{m}) = \boldsymbol{L} = \overline{p_1 - p_2}$. Depending on the line orientation, $\boldsymbol{m}$ is reflected so that the former is always true, i.e. final line profile is the submatrix diagonal.

2.4. Gamma analysis

Profeel includes gamma analysis for 1D and 2D data. The gamma index computation is performed for each data point by minimizing the squared sum of the gamma components (DTA, DD) relative to their respective gamma criteria. Gamma indices for are calculated as presented in Eq. (1)

$$\gamma(r_m) = \min\{\Gamma(r_m,\ r_c)\}\forall\{r_c\} \tag{1}$$

where r_m and r_c refer to the measured and calculated spatial locations and where

$$\Gamma(r_m,\ r_c) = \sqrt{\frac{|r_c - r_m|^2}{\Delta d_m^2} + \frac{|D_c(r_c) - D_m(r_m)|^2}{\Delta D_m^2}} \tag{2}$$

In Eq. (2), $|D_c(r_c) - D_m(r_m)|^2$ is the squared difference between measured and calculated doses (target and reference), and Δd_m mand ΔD_m are the DTA and DD criteria, respectively. [10] Profeel uses an open-source gamma computation function to compute the final gamma indices [11]. Additionally, DTA and DD can be computed with the gamma indices or DTA and DD computation can be performed alone. DTA and DD are computed independently from the gamma function.

2.4.1. Data preparation for gamma analysis

Profeel prepares the data for gamma computation by automatically matching the spatial dimensions between the two datasets by truncating the largest axes. Hence, analysed input data does not have to have the same spatial dimensions. Both datasets are also interpolated to the same resolution, if their physical sampling dimensions disagree, so that gamma, DTA and DD can be computed for each data point. The default sampling resolution is equal to the dataset with lower resolution, but the used resolution can be modified by the user.

The gamma analysis results are sensitive to the statistical fluctuations present in MC dose distributions, as described by Graves

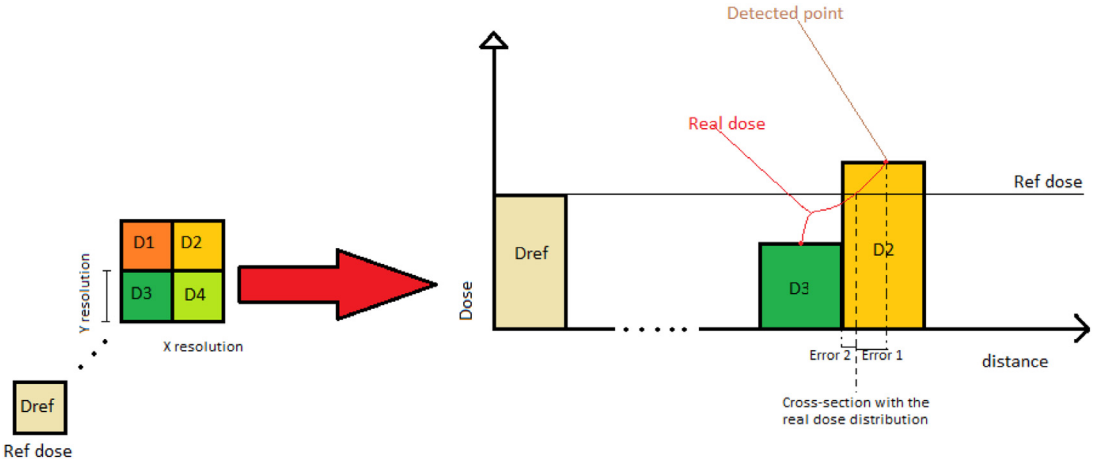

Fig. 1. 2D DTA computation error due to finite sampling.

et al. [12] Therefore the user of Profeel has an option to apply the smoothing prior to gamma analysis and to choose whether to use MC dose distribution as reference or as evaluation dataset. Additionally, the user can use custom functions to operate both input datasets along with several different normalization options (section 3.1).

2.5. Error determination due to finite grid sampling

Finite sampling introduces error to the computed DTAs, which further transfers to the gamma-indices. The user is informed about the error in the DTA result legend. The origin of the error is presented in Fig. 1.

DTAs are computed within a moving neighbourhood on a surface $S \subset \mathbf{Z}^2$: for which, function f: $S \rightarrow \mathbf{R}$ and reference dose point $c \in$ R. Let's define the neighbourhood H s.t.

$$H := \{(r_1, r_2) \in S | \|r_1 - r_2\| \leq (f(r_1) - c) \cdot (f(r_2) - c) < 0\}, \quad (3)$$

where maximum error within the neighborhood becomes $\xi = \|r_2 - r_1\| = \sqrt{2} \cdot resolution_{x,y}$, for spatially isotropic square grids. As demonstrated in Fig. 1, the spatial order of *D2* and *D3* from the reference dose is known, thus the actual DTA must lie within ξ from *D2*. This only accounts for error due to finite grid sampling in DTA algorithm.

3. Results

Profeel open-source project was originally created as a supportive tool for intuitive dosimetry data comparison and analytics between different data sources used in radiotherapy quality assurance (QA). Subsequently project development has been directed towards research purposes. The project was initialized in 2020 at the Department of Oncology at Tampere University Hospital (Tays).

3.1. Supported data types

Profeel (v. 1.17) supports several different data types, including commonly used dosimetry measurement equipment outputs in radiotherapy QA, and computed or simulated output file formats listed in Table 1

There are no limitations for the number of imported data other than set by the amount of computer memory. All datatypes are reconstructed to common structural form (.mat), containing raw, processed, result, parent reference and metadata fields.

Lower dimension data can be extracted from higher dimensions, i.e. 2D and 1D from 3D and 1D from 2D. Available data normalizations are presented in Table 2.

Table 1
Supported data types in Profeel.

Data type	Extension
PTW beamscan exports	.mcc
IBA Omnipro exports	ASCII, .OmniIMRT, .opg
PTW software exports	ASCII
EGSnrc output files	.3ddose.dcm
DICOM RT RD dose files	
Matlab structures compatible with Profeel (previous sessions)	.mat

Table 2
Normalizations in profeel.

Normalization type	Applicable data
No normalization	1D, 2D 3D
Normalization to maximum	1D, 2D 3D
Normalization to central axis (CAX)	1D
Distance percentMean value from range	1D1D
Normalization to value	1D, 2D 3D

All data with the same dimensionality can be visualized and processed simultaneously as presented in Fig. 2.

Profeel offers several data processing and analysis tools with varying flexibility, and data and result exportation in .mat and .csv formats for further processing and analysis. Data saved in .mat form is equivalent to saving the work session and can be imported to Profeel as such.

3.2. User interface

The Profeel graphical user interface (GUI) is built in the Matlab (MathWorks Inc., MA) R2020a graphical user interface development environment (GUIDE). Profeel GUI is presented in Fig. 3, for which, the GUI object groupings are presented in Table 3.

The UI figure, visualizing the data is referred as the 'main figure'. After data import, the data chosen from group b) is presented in the main figure. In the example in Fig. 3, a 3D DICOM RT dose dataset is chosen. 3D data is saved during import to a Matlab structure as 2D stacks, which can be navigated through with the mouse scroll wheel. 2D and 3D data are always presented as 2D slices/planes in Profeel.

3.3. Data processing tools

Data processing tools are mainly located in GUI grouping c), under the 'Main data processing panel'. The panel includes sub-

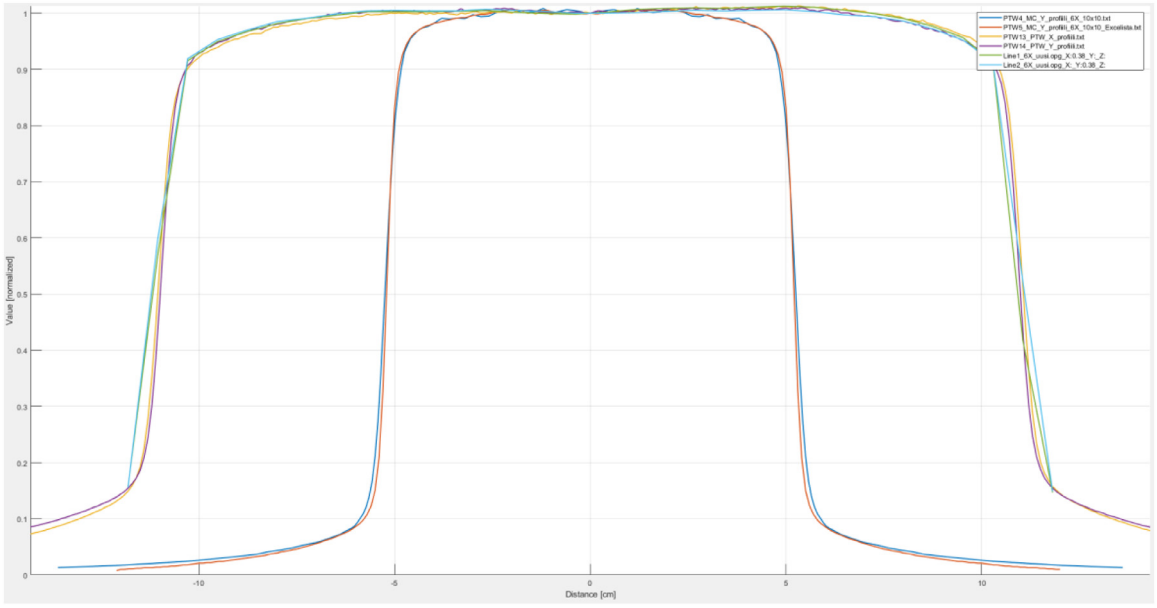

Fig. 2. Simultaneous visualization of measured and simulated dose profiles.

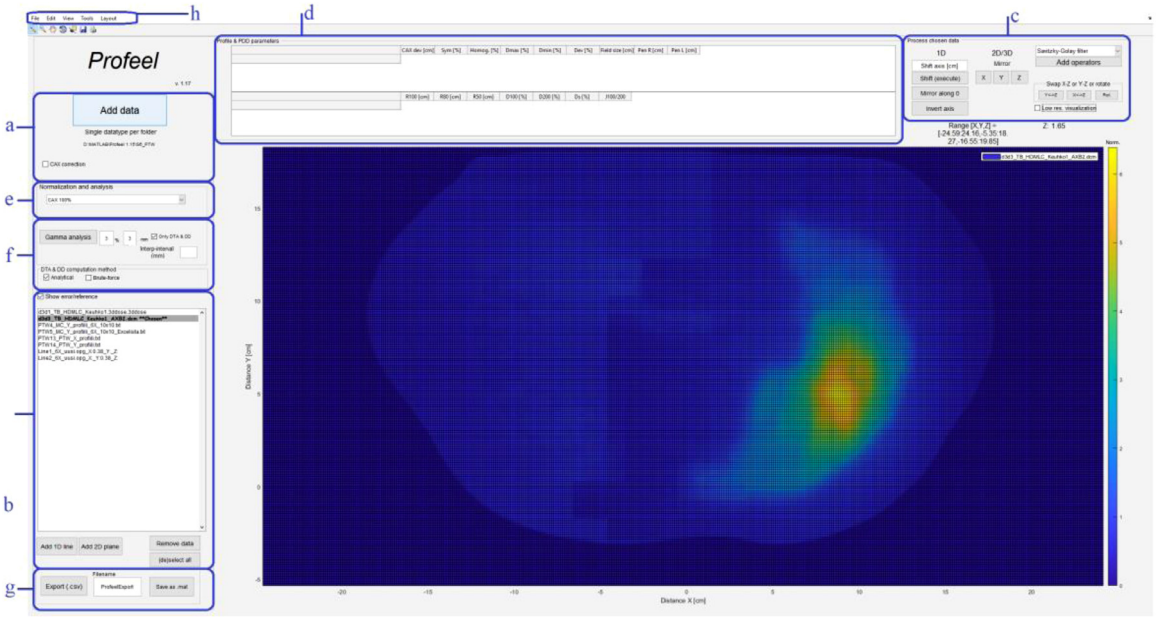

Fig. 3. Profeel user interface.

Table 3
Profeel GUI groupings in Fig. 3.

GUI group name	Description
a) Data import panel	Data import button and 1D CAX correction during import
b) Imported data listbox	Contains all imported data. Data is activated by mouse click.
c) Main data processing panel	Orientation, scaling, data filtering and custom operations
d) Profile and PDD parameters(See chapter 3.4)	Shows automatically computed 1D profile and PDD parameters
e) Data normalization panel	Different normalizations (see Table 2)
f) Gamma, DTA and DD panel	Gamma analysis tools
g) Data exportation panel	.csv and .mat data export
h) Tool ribbon	Additional and future tools

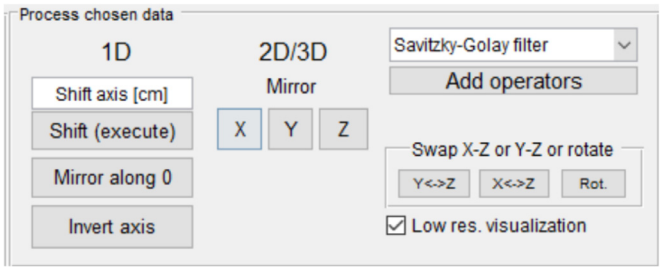

Fig. 4. Data processing GUI panel.

sections consisting of 1D and 2D/3D standard tools, such as data mirroring, inversion, rotation, shifting operator and low resolution visualization. Under the drop down menu in the upper right corner of Fig. 3 are additional processing tools, i.e. Savitzky-Golay smoothing filter for 1D and 2D data [13] and a data scaling tool (1D, 2D and 3D) as presented in Fig. 4.

Under the dropdown menu is located the 'Add operators' GUI button, which allows the user to use custom processing functions via Matlab syntax. The creation of custom processing files (ASCII) is described in detail in the Profeel Git repository's documentation [14]. Custom processing functions are applicable for all imported data types in all 3 dimensions. All front end processing operations are implemented directly on chosen data and visualized in the GUI main figure.

The data normalization drop down menu is placed under the normalization panel (GUI group e), under the import button. Data normalization options are described in section 3.1 and more details, if required, are explained in the Profeel documentation [14].

Data extraction refers to the extraction of lower dimension data from higher dimensions as described in section 2. Extraction options appear inside group b), under the listbox object after the given data is activated. After choosing the extracted dimensionality, the user inputs the extracted axis and the range to a pop-up prompt as show in Fig. 5.

If the user wants to inspect line profiles from the 2D data before 1D extraction, an interactive quick profile tool can be used, presented in Fig. 6.

Quick profile is chosen from the 'Quick profile' button included in the GUI group b). The button is visible only for applicable data (2D). If the user has performed gamma or DTA and DD analysis for the given data, the resultant profile is presented as the 2nd axis as seen in Fig. 6.

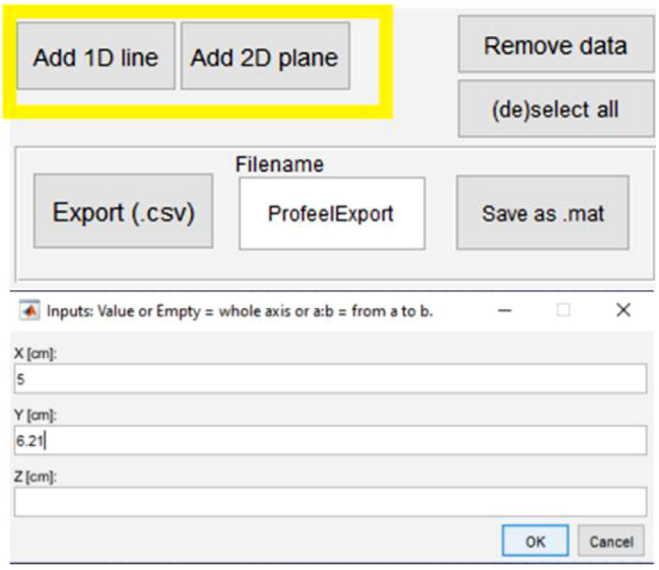

Fig. 5. Lower dimension data extraction button locations and the input prompt pop-up for lower dimension data extraction.

3.4. Data analysis tools

3.4.1. Profile and PDD parameters

Data analysis options and tools are distributed within GUI groupings d), f), h), and b) in Fig. 3, where the group d) contains the profile and PDD parameters. Profeel classifies the 1D curve types automatically during import and lower dimension extraction. The automatic curve type recognition is based on the curve symmetry and field size. The user may also re-assign the curve type under the tool ribbon (group h), which forces the program to compute the assigned parameters. Profile and PDD parameters are computed based on IEC standard 60976 [15]. The profile and PDD parameters are listed in Table 4 and 5, respectively.

Flattened region for profiles is defined only for field sizes larger or equal to 5 cm in the IEC Standard 60976. Currently Profeel has no explicit definition for field sizes below 5 cm, thus the flattened region is computed as for 5 cm≤Field size≤10 cm. [15]

If any of the parameter computation fails or profile field size is outside of the IEC confines, a descriptive warning message is printed to the program terminal.

Table 4
Profile parameters.

Parameter name [unit]	Explanation
CAX dev [cm]	Offset between computed CAX and data position axis 0-point. Computed CAX is derived from the computed field size as the symmetric center
Sym [%]	Profile symmetry is defined inside the flattened region as max(d(x)/d(-x)), where d(x) refers to the dose value at point x.
Dmax [%]	Relative maximum dose to CAX within the flattened region
Dmin [%]	Relative minimum dose to CAX within the flattened region
Dev [%]	Dose deviation between CAX and the minimum dose within the flattened region
Fieldsize [cm]	Fieldsize is defined at 50% dose value around the CAX
PenR & PenL [cm]	Right and left side penumbras, defines as the distance between 80% and 20% dose values from CAX

Table 5
PDD parameters.

Parameter name [unit]	Explanation
R100, R80, R50 [cm]	100%, 80% and 50% relative to maximum dose depths from the surface, respectively.
D100, D200 [%]	Relative doses at depths of 10 and 20 cm from the surface, respectively.
Ds [%]	Surface dose relative to the maximum dose. Surface is defined as the depth of 0.05mm in the IEC 60976.
J100/J200	Dimensionless quality parameter. Ratio between doses at 10 and 20 cm, respectively

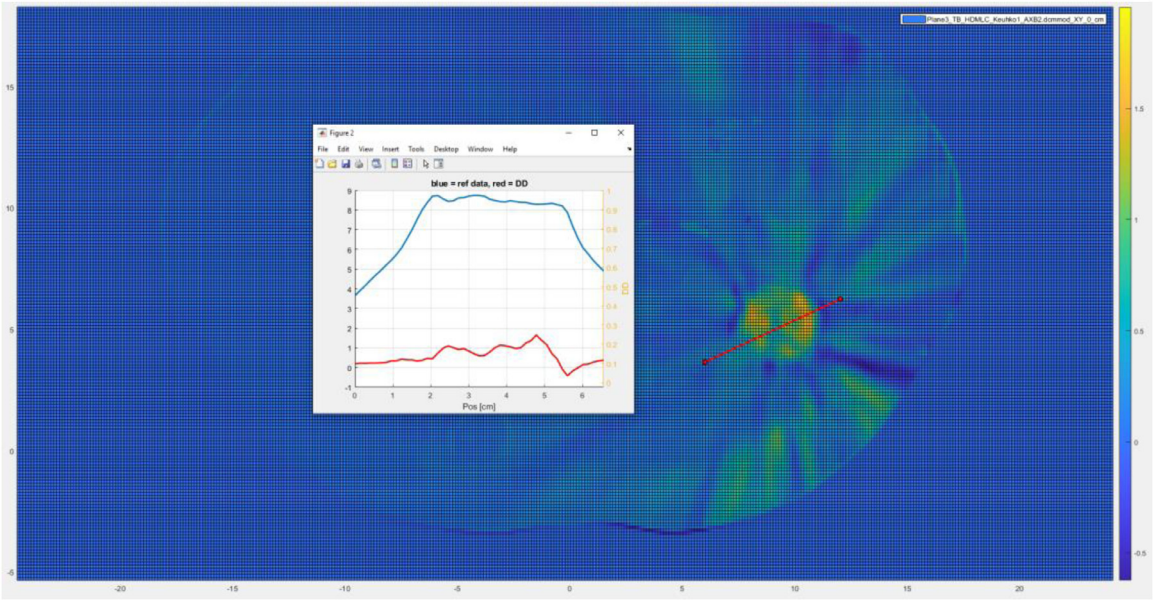

Fig. 6. Quick profile tool for fast profile inspection.

3.4.2. Gamma, DTA and DD analysis

Gamma, DTA and DD analysis are performed after the user has set required parameters in the UI panel f). First, the user selects the data (1D or 2D), so that the reference data is selected first. Gamma criteria are set as default to 3% (DD) and 3 mm (DTA), but the values can be modified by the user preceding the gamma analysis from the respective edit fields. Gamma interpolation resolution defaults to the lower resolution data by default, but can also be changed from the 'interp-interval' edit field, located in the UI group e), which will perform linear interpolation using the requested resolution. The gamma, DTA and DD computations are executed for the whole data area by default, but the user may change the analysis area by setting an isodose level from isodose edit field, which limits the computation to doses equal, or higher to the set level as presented in Fig. 7.

Gamma, DTA and DD results are shown automatically in the main figure legend after computation. The legend is located by default in the north-east corner of the figure. For 1D data, all chosen line profiles and pass percentages are presented in the legend, i.e. target data, reference data, brute force computation results and analytical computation results consisting of DTA, relative DD and absolute DD.

2D pass percentages are presented similarly in the main figure legend, but 2D distributions can only be viewed when reference data (data which was chosen 1st to the analysis) is activated. Gamma, DTA or DD distribution can be chosen from UI group b) from respectively named buttons. Additionally, the quick profile tool can be used to inspect the results against the dose profile in 1D.

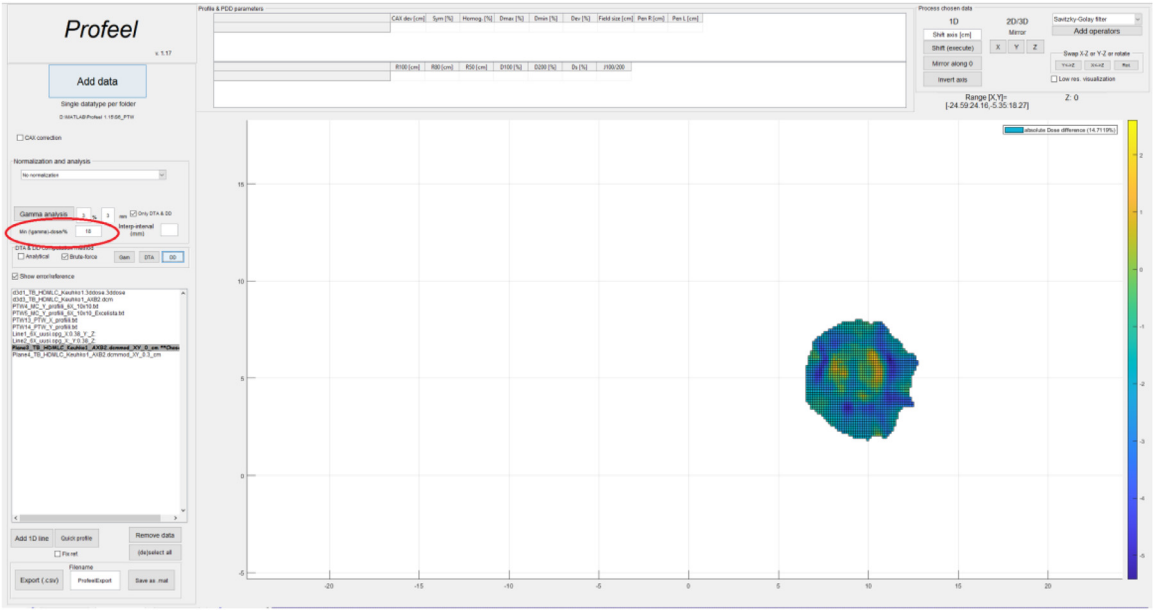

Fig. 7. Isodose delineated DD distribution.

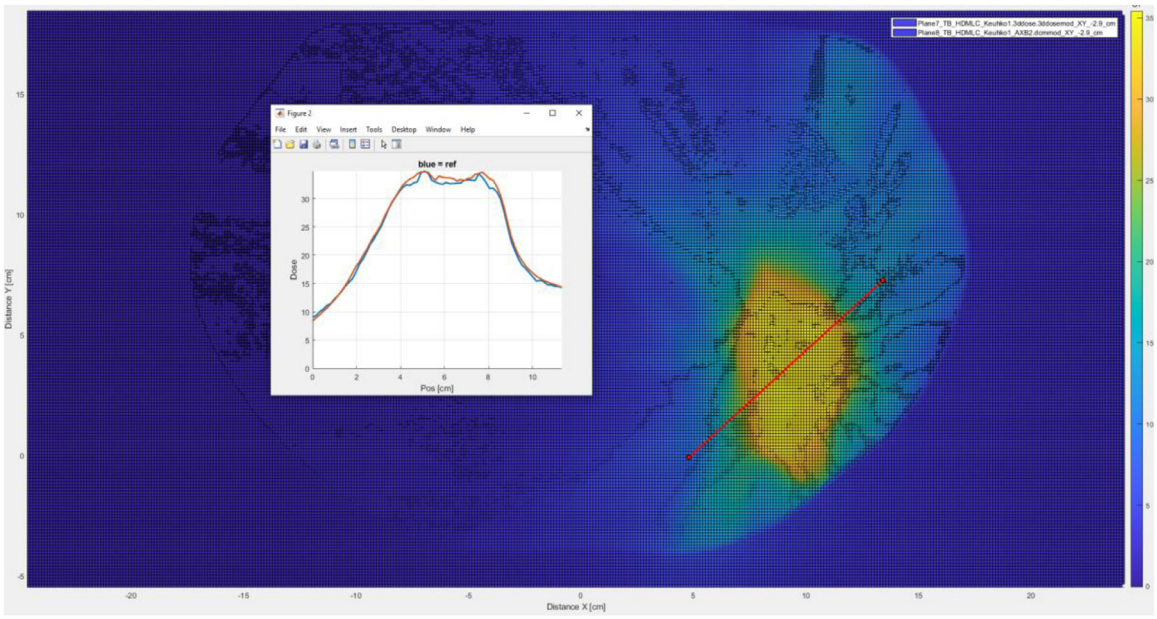

Fig. 8. Quick profile comparison between the Eclipse treatment plan and Monte carlo simulated dose data, before gamma analysis.

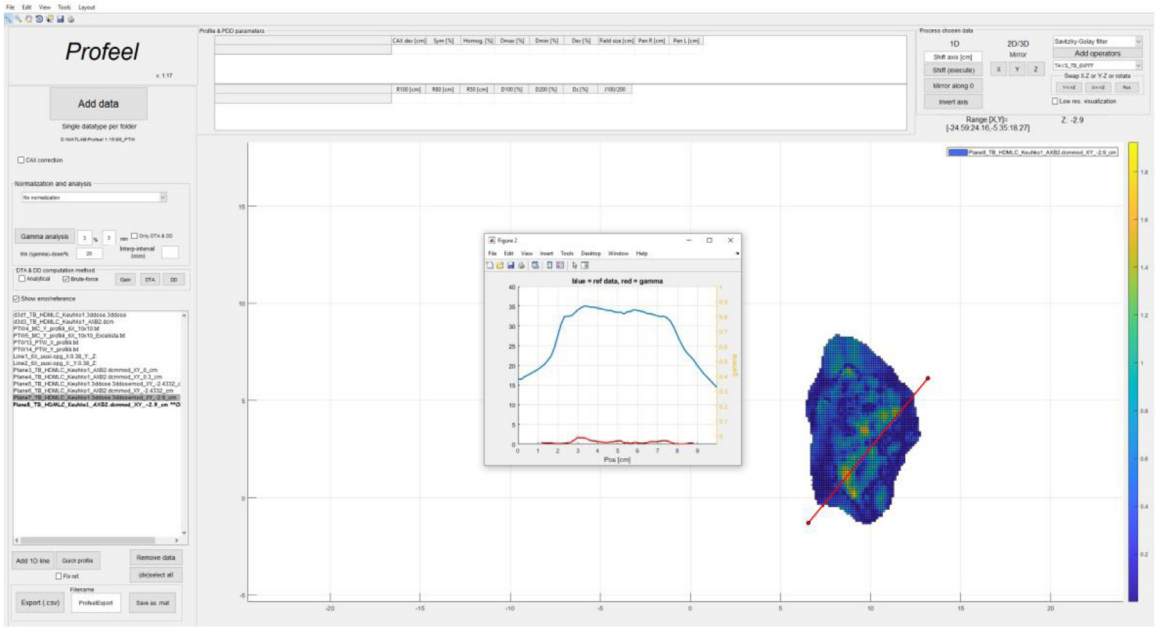

Fig. 9. Gamma distribution inspection with the quick profile tool.

Gamma, DTA and DD results can be exported to .mat or .csv format from the export buttons shown in Fig. 5. .mat format contains all data in the saved structure including the results, but the .csv format exports only the 1D normalization and interpolated data with the results. For 2D data, only final gamma, DTA and DD pass percentages are exported during .csv export.

3.5. Sample run

Sample run was performed with a DICOM RT export of volumetric modulated arc (VMAT) plan from Eclipse TPS (version 13.6) (Varian Medical Systems Inc., Palo Alto, CA, USA) and Monte Carlo simulated .3ddose data for the same case. After import, the units of the .3ddose data set were scaled using known calibration information for the simulated treatment machine. The dose scaling function and constants were first added in a custom function ASCII file, which was then operated on the 3D dataset via a custom function tool in Profeel (GUI group C). Next, proper transversal slices for analysis were searched, inspected with the quick profile tool and extracted from both datasets. The quick profile inspection is presented in Fig. 8

No additional normalization was chosen, since in this case proper dose calibration data was available. Next 2D gamma analysis was performed for the data with 20 Gy isodose limit and the default 3 mm DTA and 3% dose difference criteria. With this configuration, the 2D gamma pass percentage was found to be 94.35% with 79,9% DTA and 60.9% dose difference pass percentages. The individual gamma and gamma component maps were then inspected with the quick profile tool, which overlays the gamma results with the dose distribution as shown in Fig. 9.

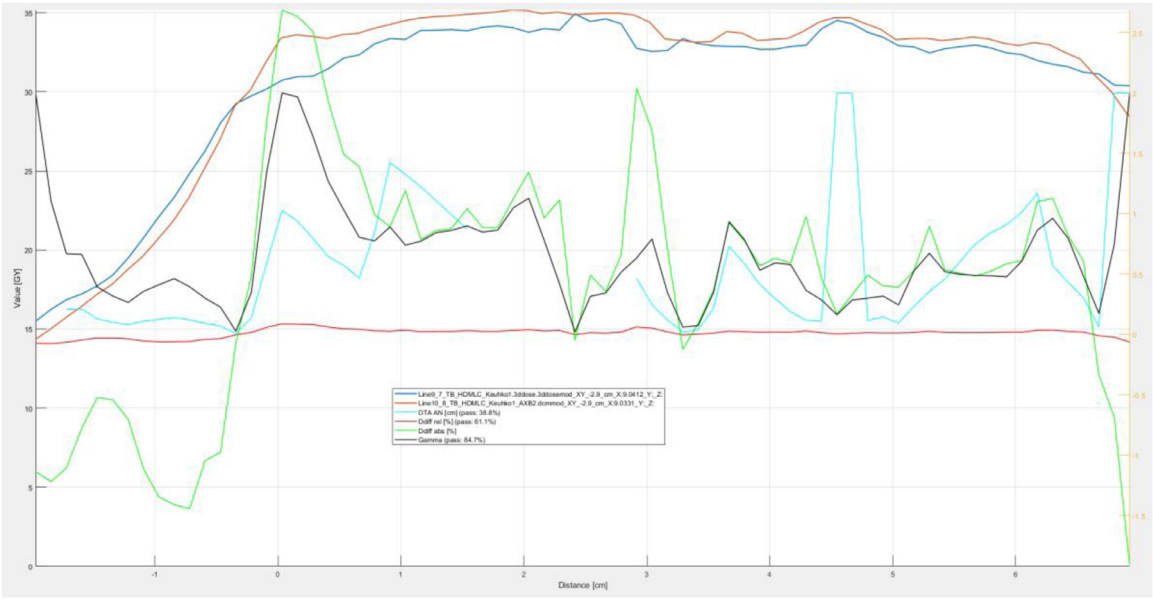

Fig. 10. Gamma analysis results for 1D comparison.

	A	B	C	D	E	F
1	Ref: Line9_7_TB_HDMLC	Target: Line10_8_TB_HDMLC_Keuhko1_AXB2.dcmmod_XY_-2.9_cm_X:				
2	Pos	dtaA(39%)	absDD	rDD (61%)	gamma (85%)	
3	-1,97104454		-1,136198716	-0,073382445	2	
4	-1,845724105		-1,219324515	-0,075084027	1,105095983	
5	-1,72040367	0,20714695	-1,105713611	-0,065615468	0,668098152	
6	-1,595083235	0,209554555	-0,774133557	-0,044970565	0,661675096	
7	-1,4697628	0,129442808	-0,523176219	-0,029515507	0,393660903	
8	-1,344442365	0,100654179	-0,540365874	-0,029370493	0,318317264	
9	-1,21912193	0,081427622	-0,700800012	-0,035981239	0,265206039	
10	-1,093801495	0,10886111	-1,111777788	-0,053562382	0,356312841	
11	-0,96848106	0,125636398	-1,345399743	-0,060880947	0,411457568	
12	-0,843160625	0,141504177	-1,409880313	-0,060418046	0,462216645	
13	-0,71784019	0,120382196	-1,442130232	-0,058064474	0,394235134	
14	-0,592519755	0,092218071	-1,043918257	-0,039760217	0,300284475	
15	-0,46719932	0,069051994	-0,976272787	-0,034833104	0,226314455	
16	-0,341878885	0,007590012	-0,073765627	-0,002522323	0,026672181	
17	-0,21655845	0,1344964	0,481502985	0,016192325	0,347015887	
18	-0,091238015	0,592679754	1,771077157	0,058688352	1,347252488	
19	0,03408242	1,026473278	2,686825986	0,087437407	2	
20	0,159402855	0,939406614	2,633843358	0,085083396	1,966935635	
21	0,28472329	0,792376188	2,510004398	0,081017955	1,640243411	
22	0,410043725	0,644060877	1,927228954	0,061262119	1,265764713	
23	0,53536416	0,570540697	1,491624477	0,046423796	1,031000853	
24	0,660684595	0,466317742	1,38882086	0,042958143	0,804754019	

CAX normalization | Not normalized | Mean normalization | Gammadata

Fig. 11. Exported 1D analysis results in .csv form.

After the inspection, limited range Y-axis 1D profiles were further extracted and both data were filtered with Savitzky-Golay filter (UI group C), with 3th polynomial order for 6 frame window size. Filtered profiles with gamma results are shown in Fig. 10.

Finally, the results were exported as .mat and in .csv form. Fig. 11. presents a typical .csv export file.

4. Discussion

Profeel is a software, where 1D/2D/3D dose distributions, whether calculated or measured, of multiple formats can be imported, processed and analyzed. Number of free-to-use and open source programs are focusing on the dosimetric analysis in radiotherapy, but unfortunately the comparison between measured and simulated data is often inaccessible without extensive preprocessing. Thus, Profeel focuses mainly on this issue. Typical example of use is to import calculated dose distribution from a clinical TPS and independent Monte Carlo simulation result and measured dose distribution. The data can be visualized and also lower dimensional (3D to 2D or 2D to 1D) sub-data from the original data can be extracted. This is essential, since normally the dose distributions are calculated in 3D, but the measurements and thus the data analysis and comparison are performed in 2D or 1D. There are multiple options for data processing, including smoothing, analysis and comparison tools. The simplest comparison is to evaluate the dose difference, but the more complex the dose distribution, more advanced metrics, such as gamma analysis are favoured. Finally, the data can be saved or exported for further use. Support for new data formats, tools for data processing and analysis/comparison and other options in the software can be added through improvement requests in Profeel GitHub repository.

In future, Profeel continues supporting medical physicists and scientists in dosimetry analysis and research. Thus far Profeel has shown to be an agile tool for fulfilling various needs of several researchers and since Profeel is under constant development and as an open source project, community needs, issues and bug reports are taken into account in the development. Profeel is not intended, and should not be used in clinical practice.

There are several areas that should be covered in future development, such as a broader range of importable data types/formats, e.g. other Monte Carlo codes, more advanced analysis tools, especially in 3D (e.g. DVH calculation, radiobiological modelling), CT and MRI image import with dosimetric data registration, extension of gamma analysis and Savitzky-Golay smoothing filter to 3D, DICOM-RT structure import and overlay and extensive program verification and validation. Also, spline interpolation for gamma analysis and gamma parameter reports should be included as described by Hussein et al. [16]. Additional known limitation is the Matlab GUIDE environment, which will become obsolete in future Matlab releases. Profeel can be still run in newer Matlab versions but to edit UI tools, the GUI must first be migrated to Matlab App Designer (MathWorks Inc., MA). The specific instructions to run Profeel, with required Toolboxes are described in the Profeel documentation [14]. All known program bugs and issues are reported to the Profeel Github repository at: https://github.com/TPakar/Profeel/issues.

Acnowledgemenets

Authors have no competing interest to declare. This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

References

[1] J. Deasy, A. Blanco, V. Clark, CERR: a computational environment for radiotherapy research, Med Phys 30 (5) (2003 May) 979–985 PMID: 12773007, doi:10.1118/1.1568978.
[2] C Pinter, A Lasso, A Wang, D Jaffray, G. Fichtinger, SlicerRT: radiation therapy research toolkit for 3D Slicer, Med Phys 39 (10) (2012 Oct) 6332–6338 PMID: 23039669, doi:10.1118/1.4754659.
[3] Omer, H., Alzimami, K. and Sulieman, A., "XSTING, Software for Evaluation of Radiotherapy Planning Performed Using EGSnrcMP Codes", Current Medical Imaging. 2014 10: 48. doi: 10.2174/1573405610011404241452O6.
[4] JY Park, JW Lee, KS Choi, JS Lee, YH Kim, S Hong, TS Suh, Development of a novel quality assurance system based on rolled-up and rolled-out radiochromic films in volumetric modulated arc therapy, Med Phys 38 (12) (2011 Dec) 6688–6696 PMID: 22149851, doi:10.1118/1.3659706.
[5] H Wang, Q Liu, D Wan, J Xiang, L Du, Y Wang, J Cao, Y Fu, F Fan, M. Hecker, BioDoser: improved dose-estimation software for biological radiation dosimetry, Comput Methods Programs Biomed 108 (1) (2012 Oct) 402–406 Epub 2012 Apr 14. PMID: 22503129, doi:10.1016/j.cmpb.2012.03.010.
[6] H.-P. Wieser, E. Cisternas, N. Wahl, S. Ulrich, A. Stadler, H. Mescher, L.-R. Müller, T. Klinge, H. Gabrys, L. Burigo, A. Mairani, S. Ecker, B. Ackermann, M. Ellerbrock, K. Parodi, O. Jäkel, M Bangert, Development of the open-source dose calculation and optimization toolkit matRad, Med. Phys. 44 (2017) 2556–2568, doi:10.1002/mp.12251.
[7] Sang-Won Kang, Jin-Beom Chung, Kyeong-Hyeon Kim, Ji-Yeon Park, Hae-Jin Park, Woong Cho, Sven Olberg, Tae Suk Suh, Justin Park, Development of Volumetric Independent Dose Calculation System for Verification of the Treatment Plan in Image-Guided Adaptive Brachytherapy, Frontiers in Oncology (2020) 10.609.10.3389/fonc.2020.00609.
[8] Martinov, M., Thomson, M. 3ddose_tools, v. 1.1, GitHub repository. 2016. Retrieved from https://physics.carleton.ca/clrp/3ddose_tools/3ddose-tools [Accessed 28.4.2021].
[9] Badum, E. VICTORIA - Voxel Interactive Contour Tool for Online Radiation Intensity Analytics. 2021. Retrieved from http://web.uvic.ca/~bazalova/dose_viewer [Accessed 28.4.2021].
[10] DA Low, WB Harms, S Mutic, JA. Purdy, A technique for the quantitative evaluation of dose distributions, Med Phys 25 (5) (1998) 656–661, doi:10.1118/1.598248.
[11] Geurts, M. CalcGamma, GitHub repository. 2014. Retrieved from https://github.com/mwgeurts/gamma [Accessed 5.8.2020].
[12] YJ Graves, X Jia, SB. Jiang, Effect of statistical fluctuation in Monte Carlo based photon beam dose calculation on gamma index evaluation, Phys Med Biol 58 (6) (2013 Mar 21) 1839–1853 Epub 2013 Feb 27. PMID: 23442443, doi:10.1088/0031-9155/58/6/1839.
[13] MathWorks. 2020. Matlab Documentation - Savitzky-Golay filtering. Retrieved from https://se.mathworks.com/help/signal/ref/sgolayfilt.html [Accessed 9.4.2021].
[14] T. Pakarinen, J.Profeel Ojala, Open Source Dosimetry Data Visualization and Analytics Software, v. 1.17, GitHub repository (2020). [Accessed 9.4.2021]. https://github.com/TPakar/Profeel.
[15] IEC - International Electrotechnical Commission, Medical electrical equipment - Dosimeters with ionization chamber as used in radiotherapy, IEC Standard 60976 (2011) Genève: IEC.
[16] M Hussein, CH Clark, A. Nisbet, Challenges in calculation of the gamma index in radiotherapy - Towards good practice, Phys Med 36 (2017 Apr) 1–11 Epub 2017 Mar 14. PMID: 28410677, doi:10.1016/j.ejmp.2017.03.001.